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OI 10 IntelliGenetics
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Multiple Sequence Alignment Program
Case 5.4

Thu 21 Feb 102 14:54:03-PST

Solution Parameters:

Amino Alphabet = Identity
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off
AMINO-Res-length = 2
Deletion-weight = 5.00
Length-factor = 0
Matching-weight = 1.00
JCLEIC-Res-length = 4
read-factor = 50

Clustered order of selected sequences:

1. HARRIS-EDG4.PEP (1-382)
2. US-09-274-752D-1 (1-382)

Region Alignment: (listed in Clustered order)

HARRIS-EDG 1 MVIMGQCYNETIGFFYNNSGKELSHWRPKDVVVALGLTVSVLVLLTNLLVIAAIAASNR
US-09-274- 1 MVIMGQCYNETIGFFYNNSGKELSHWRPKDVVVALGLTVSVLVLLTNLLVIAAIAASNR
consensus
HARRIS-EDG 62 RFHPIYYLLGNLAADLFAGVAYLFLMFHTGPTARLSLEGWFLRQGLDTSLTASVATL
US-09-274- 62 RFHPIYYLLGNLAADLFAGVAYLFLMFHTGPTARLSLEGWFLRQGLDTSLTASVATL
consensus
HARRIS-EDG 123 LAIAVERHRSYMAVOLHSRLPRGRVVMILIVGVVAAALGLGLLPAHSHWHCLCALDRCRMAP
US-09-274- 123 LAIAVERHRSYMAVOLHSRLPRGRVVMILIVGVVAAALGLGLLPAHSHWHCLCALDRCRMAP
consensus
HARRIS-EDG 184 LLSRSYLAVWALSLLVFLLMVAVYTRIFFYVRRRVQSMAEHVSCHPRYRETTLSLVKTIV
US-09-274- 184 LLSRSYLAVWALSLLVFLLMVAVYTRIFFYVRRRVQSMAEHVSCHPRYRETTLSLVKTIV
consensus
HARRIS-EDG 245 IILGAFVVCWTPPGQVLLLDGLGCESCNAVLAVERKYLFLLAELANSLVNAAVYSCRDsEMRRT
US-09-274- 245 IILGAFVVCWTPPGQVLLLDGLGCESCNAVLAVERKYLFLLAELANSLVNAAVYSCRDsEMRRT
consensus
HARRIS-EDG 306 FRLLCCACLRQSTRESVHTSSAOGGASTRIMLPENGHPMLTPPFYSYLELQRYAASNKST
US-09-274- 306 FRLLCCACLRQSTRESVHTSSAOGGASTRIMLPENGHPMLTPPFYSYLELQRYAASNKST
consensus

HARRIS-EDG 367 APDDLWVLLAQPNOOD
US-09-274- 367 APDDLWVLLAQPNOOD
consensus APDDLWVLLAQPNOOD

Alignment score = 380.00

Scoring matrix:

| | | |
|---|-----|---|
| | 1 | 2 |
| 1 | 380 | |
| 2 | | |